

80520

113

STIC-Biotech/ChemLib

187945

From: Bowman, Amy  
Sent: Monday, May 01, 2006 5:09 AM  
To: STIC-Biotech/ChemLib  
Cc: Bowman, Amy  
Subject: sequence search-SEQ ID 82

Hello,  
I need a search of SEQ ID NO: 82 in application 10/605,498, length limited to 35 nucleotides.  
I need to include an interference search.

Thank you,  
Amy Bowman  
AU 1635  
REM 2C31  
mail REM 2C18  
571-272-0755

BEST AVAILABLE COPY

\*\*\*\*\*

Searcher: Jan  
Searcher Phone: 122504  
Date Searcher Picked up: 518104  
Date completed: 518106  
Searcher Prep Time: 10  
Online Time: 15

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Type of Search  
NA# ✓ AA#:           
S/L:          Oligomer:           
Encode/Transl:           
Structure #:          Text:           
Inventor:          Litigation:         

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Vendors and cost where applicable  
STN:           
DIALOG:           
QUESTEL/ORBIT:           
LEXIS/NEXIS:           
SEQUENCE SYSTEM: ✓  
WWW/Internet:           
Other (Specify):

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1
AUTHORS Gleave,M.E., Rocchi,P. and Signaevsky,M.
TITLE Compositions for treatment of prostate and other cancers
JOURNAL Patent: WO 2004030660-A 81 15-APR-2004;
The University of British Columbia (CA)
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ACCESSION CQ799992
VERSION CQ799992.1 GI:46848939
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1
AUTHORS Gleave,M.E., Rocchi,P. and Signaevsky,M.
TITLE Compositions for treatment of prostate and other cancers
JOURNAL Patent: WO 2004030660-A 90 15-APR-2004;
The University of British Columbia (CA)
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/mol_type="unassigned RNA"
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ACCESSION CQ799905
VERSION CQ799905.1 GI:46848952
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1
AUTHORS Gleave,M.E., Rocchi,P. and Signaevsky,M.
TITLE Compositions for treatment of prostate and other cancers
JOURNAL Patent: WO 2004030660-A 3 15-APR-2004;
The University of British Columbia (CA)
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Db 1 CCGCGCGCTCGGTTCAT 16
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LOCUS CQ799906 21 bp DNA linear PAT 28-APR-2004
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ACCESSION CQ799906
VERSION CQ799906.1 GI:46848853
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1
AUTHORS Gleave,M.E., Rocchi,P. and Signaevsky,M.
TITLE Compositions for treatment of prostate and other cancers
JOURNAL Patent: WO 2004030660-A 4 15-APR-2004;
The University of British Columbia (CA)
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LOCUS AR559501 33 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 16 from patent US 6750042.
ACCESSION AR559501
VERSION AR559501.1 GI:53968947
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Summers,A.O. and Caguiat,J.J.
TITLE Metal binding proteins, recombinant host cells and methods
JOURNAL Patent: US 6750042-A 16 15-JUN-2004;
University of Georgia Research Foundation, Inc.; Athens, GA
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 DEFINITION Sequence 14 from patent US 6784346.  
 ACCESSION AR579704  
 VERSION AR579704.1 GI:56583159  
 KEYWORDS .  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 24)  
 AUTHORS Cho, M.-J., Lemaux, P.G., Buchanan, B.B., Wong, J. and Marx, C.  
 TITLE Value-added traits in grain and seed transformed with thioresdoxin  
 JOURNAL Patent: US 6784346-A 14 31-AUG-2004;  
 The Regents of the University of California; Oakland, CA  
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 Db 19 GCACGAGCGCTCGGATAT 1

Search completed: May 8, 2006, 09:47:45  
 Job time : 1776 secs

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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2006, 09:56:51 ; Search time 602 Seconds  
(without alignments)  
274.730 Million cell updates/sec

Title: US-10-605-498-82

Perfect score: 20  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 10726526

Minimum DB seq length: 0  
Maximum DB seq length: 35

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_NA\_Main:\*

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- 3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
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- 7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	20	100.0	21	7	US-10-605-498-81
3	19	95.0	19	7	US-10-605-498-90
4	16	80.0	21	7	US-10-605-498-3
5	15.2	76.0	25	7	US-10-719-956-135321
6	15	75.0	21	7	US-10-605-498-4
7	14.2	71.0	25	10	US-11-036-317-261850
8	14.2	71.0	25	10	US-11-036-317-269817
9	14.2	71.0	25	10	US-11-036-317-330516
10	14.2	71.0	25	10	US-11-036-317-332488
11	14.2	71.0	25	10	US-11-036-317-364465
12	14.2	71.0	25	10	US-11-036-317-406575
13	14.2	71.0	25	10	US-11-036-317-536426
14	14.2	71.0	25	10	US-11-036-317-536427
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22	13.6	68.0	25	7	US-10-719-956-198103
23	13.6	68.0	25	8	US-10-719-900-309243

24	13.6	68.0	25	10	US-11-036-317-912027	Sequence 912027,
25	13.6	68.0	25	10	US-11-036-317-912041	Sequence 912041,
c 26	13.2	66.0	25	5	US-10-098-263B-3853	Sequence 3853, Ap
27	13.2	66.0	25	5	US-10-098-263B-65789	Sequence 65789, A
28	13.2	66.0	25	7	US-10-719-956-110491	Sequence 110491,
c 29	13.2	66.0	25	7	US-10-719-956-547822	Sequence 547822,
c 30	13.2	66.0	25	7	US-10-719-956-547823	Sequence 547823,
31	13.2	66.0	25	8	US-10-719-900-148603	Sequence 148603,
32	13.2	66.0	25	8	US-10-719-900-148603	Sequence 148603,
33	13.2	66.0	25	8	US-10-719-900-849503	Sequence 849503,
34	13.2	66.0	25	9	US-10-809-189-53301	Sequence 849504,
35	13.2	66.0	25	10	US-11-036-317-321539	Sequence 53301, A
36	13.2	66.0	25	10	US-11-036-317-787134	Sequence 321539,
c 37	13.2	66.0	25	10	US-11-060-756-166335	Sequence 787134,
c 38	13.2	66.0	25	10	US-11-060-756-166384	Sequence 166335,
c 39	13.2	66.0	25	10	US-11-060-756-229339	Sequence 166384,
c 40	13.2	66.0	25	10	US-11-060-756-229340	Sequence 229339,
41	13	65.0	20	5	US-10-206-654-19	Sequence 229340,
42	13	65.0	25	7	US-10-719-956-632447	Sequence 19, Appl
43	13	65.0	25	10	US-11-036-317-883329	Sequence 632447,
44	13	65.0	25	10	US-11-036-317-937963	Sequence 883329,
45	12.8	64.0	24	5	US-10-193-692-3	Sequence 937963,
						Sequence 3, Appli

ALIGNMENTS

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US-10-605-498-82  
; Sequence 82, Application US/10605498  
; Publication No. US20040127441A1  
; GENERAL INFORMATION:  
; APPLICANT: Gleave, Martin  
; APPLICANT: Rocchi, Palma  
; APPLICANT: Signaevsky, Maxim  
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other  
; FILE REFERENCE: UBC.P-031  
; CURRENT APPLICATION NUMBER: US/10/605,498  
; PRIOR FILING DATE: 2003-10-02  
; PRIOR APPLICATION NUMBER: US 60/415,859  
; PRIOR FILING DATE: 2002-10-02  
; PRIOR APPLICATION NUMBER: US 60/463,952  
; PRIOR FILING DATE: 2003-04-18  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 82  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-605-498-82

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Best Local Similarity 100.0%; Pred. No. 5.5;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCGGTCTAT 20  
Db 1 GGGACGCGCGCTCGGTCTAT 20

RESULT 2  
US-10-605-498-81  
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; Publication No. US20040127441A1  
; GENERAL INFORMATION:  
; APPLICANT: Gleave, Martin  
; APPLICANT: Rocchi, Palma  
; APPLICANT: Signaevsky, Maxim  
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other  
; FILE REFERENCE: UBC.P-031  
; CURRENT APPLICATION NUMBER: US/10/605,498

; CURRENT FILING DATE: 2003-10-02  
; PRIOR APPLICATION NUMBER: US 60/415,859  
; PRIOR FILING DATE: 2002-10-02  
; PRIOR APPLICATION NUMBER: US 60/463,952  
; PRIOR FILING DATE: 2003-04-18  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 81  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-605-498-81

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; Publication No. US20040127441A1  
; GENERAL INFORMATION:  
; APPLICANT: Gleave, Martin  
; APPLICANT: Rocchi, Palma  
; APPLICANT: Signaevsky, Maxim  
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other  
; FILE REFERENCE: UBC.P-031  
; CURRENT APPLICATION NUMBER: US/10/605,498  
; CURRENT FILING DATE: 2003-10-02  
; PRIOR APPLICATION NUMBER: US 60/415,859  
; PRIOR FILING DATE: 2002-10-02  
; PRIOR APPLICATION NUMBER: US 60/463,952  
; PRIOR FILING DATE: 2003-04-18  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 90  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-605-498-90

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Matches 19; Conservative 0; Mismatches 0;

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; Publication No. US20040127441A1  
; GENERAL INFORMATION:  
; APPLICANT: Gleave, Martin  
; APPLICANT: Rocchi, Palma  
; APPLICANT: Signaevsky, Maxim  
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other  
; FILE REFERENCE: UBC.P-031  
; CURRENT APPLICATION NUMBER: US/10/605,498  
; CURRENT FILING DATE: 2003-10-02  
; PRIOR APPLICATION NUMBER: US 60/415,859  
; PRIOR FILING DATE: 2002-10-02  
; PRIOR APPLICATION NUMBER: US 60/463,952  
; PRIOR FILING DATE: 2003-04-18

; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn version 3.2  
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; TYPE: DNA  
; ORGANISM: Homo sapiens  
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QY 5 CGCGGGCGCTCGGTGCAT 20  
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US-10-719-956-135321/c  
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; Publication No. US20040146910A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
; FILE REFERENCE: 3527.1  
; CURRENT APPLICATION NUMBER: US/10/719,956  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,836  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 699466  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 135321  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
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US-10-605-498-4  
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; Publication No. US20040127441A1  
; GENERAL INFORMATION:  
; APPLICANT: Gleave, Martin  
; APPLICANT: Rocchi, Palma  
; APPLICANT: Signaevsky, Maxim  
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other  
; FILE REFERENCE: UBC.P-031  
; CURRENT APPLICATION NUMBER: US/10/605,498  
; CURRENT FILING DATE: 2003-10-02  
; PRIOR APPLICATION NUMBER: US 60/415,859  
; PRIOR FILING DATE: 2002-10-02  
; PRIOR APPLICATION NUMBER: US 60/463,952  
; PRIOR FILING DATE: 2003-04-18  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 21  
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; ORGANISM: Homo sapiens  
US-10-605-498-4

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 7 GGGACGGCGGCTCG 21

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; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; APPLICANT: Blume, John  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1  
; CURRENT APPLICATION NUMBER: US/11/036,317  
; CURRENT FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: US 60/536,639  
; PRIOR FILING DATE: 2004-01-13  
; NUMBER OF SEQ ID NOS: 991174  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 261850  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-036-317-261850

Query Match 71.0%; Score 14.2; DB 10; Length 25;

Best Local Similarity 84.2%; Pred. No. 3.6e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTCA 19  
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Db 3 GGGACGGCGGCTCGCCA 21

## RESULT 8

US-11-036-317-269817  
; Sequence 269817, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; APPLICANT: Blume, John  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1  
; CURRENT APPLICATION NUMBER: US/11/036,317  
; CURRENT FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: US 60/536,639  
; PRIOR FILING DATE: 2004-01-13  
; NUMBER OF SEQ ID NOS: 991174  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 269817  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-036-317-269817

Query Match

Best Local Similarity 71.0%; Score 14.2; DB 10; Length 25;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTCA 19  
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Db 5 GGGACGGCGGCTCGCCA 23

## RESULT 9

US-11-036-317-330516  
; Sequence 330516, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan

; APPLICANT: Blume, John  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1  
; CURRENT APPLICATION NUMBER: US/11/036,317  
; CURRENT FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: US 60/536,639  
; PRIOR FILING DATE: 2004-01-13  
; NUMBER OF SEQ ID NOS: 991174  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 330516  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-036-317-330516

Query Match 71.0%; Score 14.2; DB 10; Length 25;

Best Local Similarity 84.2%; Pred. No. 3.6e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTCA 19  
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Db 1 GGGACGGCGGCTCGCCA 19

## RESULT 10

US-11-036-317-332488  
; Sequence 332488, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; APPLICANT: Blume, John  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1  
; CURRENT APPLICATION NUMBER: US/11/036,317  
; CURRENT FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: US 60/536,639  
; PRIOR FILING DATE: 2004-01-13  
; NUMBER OF SEQ ID NOS: 991174  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
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; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-036-317-332488

Query Match

Best Local Similarity 71.0%; Score 14.2; DB 10; Length 25;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTCA 19  
|||||  
Db 2 GGGACGGCGGCTCGCCA 20

## RESULT 11

US-11-036-317-364465  
; Sequence 364465, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; APPLICANT: Blume, John  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1  
; CURRENT APPLICATION NUMBER: US/11/036,317  
; CURRENT FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: US 60/536,639  
; PRIOR FILING DATE: 2004-01-13  
; NUMBER OF SEQ ID NOS: 991174  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 364465  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-036-317-364465

US-11-036-317-364465

Query Match 71.0%; Score 14.2; DB 10; Length 25;  
Best Local Similarity 84.2%; Pred. No. 3.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCGGTCA 19  
|||||  
Db 4 GGGACGCGCGATCTGCCA 22

RESULT 12

US-11-036-317-406575  
; Sequence 406575, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1  
; CURRENT APPLICATION NUMBER: US/11/036,317  
; CURRENT FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: US 60/536,639  
; PRIOR FILING DATE: 2004-01-13  
; NUMBER OF SEQ ID NOS: 991174  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 406575  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-036-317-406575

Query Match 71.0%; Score 14.2; DB 10; Length 25;  
Best Local Similarity 84.2%; Pred. No. 3.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCGGTCA 19  
|||||  
Db 7 GGGACGAGCGCTTTGTCA 25

RESULT 13

US-11-036-317-536426  
; Sequence 536426, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1  
; CURRENT APPLICATION NUMBER: US/11/036,317  
; CURRENT FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: US 60/536,639  
; PRIOR FILING DATE: 2004-01-13  
; NUMBER OF SEQ ID NOS: 991174  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 536426  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-036-317-536426

Query Match 71.0%; Score 14.2; DB 10; Length 25;  
Best Local Similarity 84.2%; Pred. No. 3.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCGGTCA 19  
|||||  
Db 7 GGGACGAGCGCTTTGTCA 25

RESULT 14

US-11-036-317-536427

; Sequence 536427, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1  
; CURRENT APPLICATION NUMBER: US/11/036,317  
; CURRENT FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: US 60/536,639  
; PRIOR FILING DATE: 2004-01-13  
; NUMBER OF SEQ ID NOS: 991174  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 536427  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-036-317-536427

Query Match 71.0%; Score 14.2; DB 10; Length 25;  
Best Local Similarity 84.2%; Pred. No. 3.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCGGTCA 19  
|||||  
Db 7 GGGACGTGCGCTTTGTCA 25

RESULT 15

US-09-977-137A-16  
; Sequence 16, Application US/09977137A  
; Publication No. US20030104524A1  
; GENERAL INFORMATION:  
; APPLICANT: Summers, Anne O.  
; TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and  
; TITLE OF INVENTION: Methods  
; FILE REFERENCE: 79-00  
; CURRENT APPLICATION NUMBER: US/09/977,137A  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 60/240,465  
; PRIOR FILING DATE: 2000-10-12  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 33  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
US-09-977-137A-16

Query Match 71.0%; Score 14.2; DB 3; Length 33;  
Best Local Similarity 84.2%; Pred. No. 3.4e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCGGTCA 19  
|||||  
Db 6 GGGTCTCGCGCTCGGCA 24

Search completed: May 8, 2006, 10:41:19  
JOB time : 602 secs

Result No.	Query			Description		
	Score	Match	Length	ID	DB	
C	1	20	100.0	20	12	ADM94732
	2	20	100.0	21	12	ADM94731
	3	19	95.0	19	12	ADM94740
	4	16	80.0	21	12	ADM94653
	5	15	75.0	21	12	ADM94654
	6	14.2	71.0	33	6	ABK52211
	7	14	70.0	25	9	ACH58106
	8	13.2	66.0	25	9	ACI03862
	9	13.2	66.0	25	9	ACI65798
	10	13.2	66.0	27	4	AHH21740
C	11	12.8	64.0	21	2	AAV51704
	12	12.8	64.0	23	3	AAA75395
	13	12.8	64.0	24	8	ABZ58873
	14	12.8	64.0	25	9	ACI84537
	15	12.8	64.0	29	12	ADO31537
C	16	12.8	64.0	30	14	ADY40845
	17	12.6	63.0	20	6	ABZ08781
	18	12.6	63.0	22	10	ACD26306
	19	12.6	63.0	24	2	AAX34633
	20	12.6	63.0	24	2	AAX34633

CC composition has cytostatic activity, and can be used in gene therapy. The  
CC composition is useful in treating cancer, e.g., prostate, bladder, lung,  
CC breast, pancreatic, colon, skin (for example melanoma), renal or ovarian  
CC cancer or a central nervous system malignancy. The present sequence  
CC represents a human hsp27 antisense oligonucleotide which is used in the  
CC exemplification of the present invention.

SQ Sequence 20 BP; 2 A; 6 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCTCGGTCAAT 20  
Db 1 GGGACGGCGCTCGGTCAAT 20  
|||||

## RESULT 2

ADM94731  
ID ADM94731 standard; DNA; 21 BP.

AC ADM94731;

XX 01-JUL-2004 (first entry)

DE Human heat shock protein 27 antisense oligonucleotide SEQ ID NO:81.

XX heat shock protein 27; hsp27; cytostatic; gene therapy;

KW heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;

KW antisense oligonucleotide; ss.

XX Homo sapiens.

OS Synthetic.

XX WO2004030660-A2.

XX 15-APR-2004.

XX 02-OCT-2003; 2003WO-CA001588.

XX 02-OCT-2002; 2002US-0415859P.

PR 18-APR-2003; 2003US-0463952P.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX Gleave ME, Rocchi P, Signaevsky M;

XX WPI; 2004-316331/29.

XX New composition comprising a therapeutic agent that reduces the amount of  
PT active hsp27 in hsp27 expressing cells exposed to the therapeutic agent,  
PT useful in treating cancer, e.g., prostate cancer or a central nervous  
PT system malignancy.

XX Claim 5; SEQ ID NO 81; 38pp; English.

XX The present invention describes a composition which comprises a  
CC therapeutic agent that reduces the amount of active heat shock protein 27  
CC (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The  
CC composition has cytostatic activity, and can be used in gene therapy. The  
CC composition is useful in treating cancer, e.g., prostate, bladder, lung,  
CC breast, pancreatic, colon, skin (for example melanoma), renal or ovarian  
CC cancer or a central nervous system malignancy. The present sequence  
CC represents a human hsp27 antisense oligonucleotide which is used in the  
CC exemplification of the present invention.

SQ Sequence 21 BP; 2 A; 6 C; 10 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 21;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCTCGGTCAAT 20  
Db 2 GGGACGGCGCTCGGTCAAT 21  
|||||

## RESULT 3

ADM94740/c

ID ADM94740 standard; DNA; 19 BP.

XX ADM94740;

XX 01-JUL-2004 (first entry)

DE Human heat shock protein 27 siRNA oligonucleotide SEQ ID NO:90.

XX heat shock protein 27; hsp27; cytostatic; gene therapy;

KW heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;

KW short interfering RNA; siRNA; RNA interference; RNAi; ds.

XX Homo sapiens.

OS Synthetic.

XX WO2004030660-A2.

XX 15-APR-2004.

XX 02-OCT-2003; 2003WO-CA001588.

XX 02-OCT-2002; 2002US-0415859P.

PR 18-APR-2003; 2003US-0463952P.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX Gleave ME, Rocchi P, Signaevsky M;

XX WPI; 2004-316331/29.

XX New composition comprising a therapeutic agent that reduces the amount of  
PT active hsp27 in hsp27 expressing cells exposed to the therapeutic agent,  
PT useful in treating cancer, e.g., prostate cancer or a central nervous  
PT system malignancy.

XX Claim 10; SEQ ID NO 90; 38pp; English.

XX The present invention describes a composition which comprises a  
CC therapeutic agent that reduces the amount of active heat shock protein 27  
CC (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The  
CC composition has cytostatic activity, and can be used in gene therapy. The  
CC composition is useful in treating cancer, e.g., prostate, bladder, lung,  
CC breast, pancreatic, colon, skin (for example melanoma), renal or ovarian  
CC cancer or a central nervous system malignancy. The present sequence  
CC represents a human hsp27 short interfering RNA (siRNA) oligonucleotide  
CC which is used in the exemplification of the present invention.

SQ Sequence 19 BP; 3 A; 8 C; 6 G; 0 T; 2 U; 0 Other;

Query Match 95.0%; Score 19; DB 12; Length 19;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGACGGCGCTCGGTCAAT 20  
Db 19 GGACGGCGCTCGGTCAAT 1  
|||||

## RESULT 4

ADM94653

ID ADM94653 standard; DNA; 21 BP.

XX ADM94653;

XX 01-JUL-2004 (first entry)

DE Human heat shock protein 27 antisense oligonucleotide SEQ ID NO:3.  
XX heat shock protein 27; hsp27; cytostatic; gene therapy;  
KW heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;  
KW antisense oligonucleotide; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX WO2004030660-A2.  
XX  
XX  
PD 15-APR-2004.  
XX  
XX  
XX 02-OCT-2003; 2003WO-CA001588.  
XX  
XX 02-OCT-2002; 2002US-0415859P.  
PR 18-APR-2003; 2003US-0463952P.  
XX (UYBR-) UNIV BRITISH COLUMBIA.  
XX  
XX Gleave ME, Rocchi P, Signaevsky M;  
XX WPI; 2004-316331/29.  
XX  
XX New composition comprising a therapeutic agent that reduces the amount of  
PT active hsp27 in hsp27 expressing cells exposed to the therapeutic agent,  
PT useful in treating cancer, e.g., prostate cancer or a central nervous  
PT system malignancy.  
XX  
XX Claim 5; SEQ ID NO 3; 38pp; English.  
XX  
XX The present invention describes a composition which comprises a  
CC therapeutic agent that reduces the amount of active heat shock protein 27  
CC (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The  
CC composition has cytostatic activity, and can be used in gene therapy. The  
CC composition is useful in treating cancer, e.g., prostate, bladder, lung,  
CC breast, pancreatic, colon, skin (for example melanoma), renal or ovarian  
CC cancer or a central nervous system malignancy. The present sequence  
CC represents a human hsp27 antisense oligonucleotide which is used in the  
CC exemplification of the present invention.  
XX  
XX Sequence 21 BP; 1 A; 7 C; 9 G; 4 T; 0 U; 0 Other;  
XX  
XX Query Match 80.0%; Score 16; DB 12; Length 21;  
XX Best Local Similarity 100.0%; Pred. No. 8.2e+02;  
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 5 CGCGCGCTCGGTGCAT 20  
DB 1 CGCGCGCTCGGTGCAT 16  
XX  
RESULT 5  
ADM94654  
ID ADM94654 standard; DNA; 21 BP.  
XX  
XX ADM94654;  
XX  
XX 01-JUL-2004 (first entry)  
XX  
XX Human heat shock protein 27 antisense oligonucleotide SEQ ID NO:4.  
XX  
XX heat shock protein 27; hsp27; cytostatic; gene therapy;  
KW heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;  
KW antisense oligonucleotide; ss.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX WO2004030660-A2.  
XX  
XX 15-APR-2004.  
XX

PF 02-OCT-2003; 2003WO-CA001588.  
XX  
XX 02-OCT-2002; 2002US-0415859P.  
PR 18-APR-2003; 2003US-0463952P.  
XX (UYBR-) UNIV BRITISH COLUMBIA.  
XX  
XX Gleave ME, Rocchi P, Signaevsky M;  
XX WPI; 2004-316331/29.  
XX  
XX New composition comprising a therapeutic agent that reduces the amount of  
PT active hsp27 in hsp27 expressing cells exposed to the therapeutic agent,  
PT useful in treating cancer, e.g., prostate cancer or a central nervous  
PT system malignancy.  
XX  
XX Claim 5; SEQ ID NO 4; 38pp; English.  
XX  
XX The present invention describes a composition which comprises a  
CC therapeutic agent that reduces the amount of active heat shock protein 27  
CC (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The  
CC composition has cytostatic activity, and can be used in gene therapy. The  
CC composition is useful in treating cancer, e.g., prostate, bladder, lung,  
CC breast, pancreatic, colon, skin (for example melanoma), renal or ovarian  
CC cancer or a central nervous system malignancy. The present sequence  
CC represents a human hsp27 antisense oligonucleotide which is used in the  
CC exemplification of the present invention.  
XX  
XX Sequence 21 BP; 4 A; 5 C; 11 G; 1 T; 0 U; 0 Other;  
XX  
XX Query Match 75.0%; Score 15; DB 12; Length 21;  
XX Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 GCGACGCGCGCTCG 15  
DB 7 GCGACGCGCGCTCG 21  
XX  
RESULT 6  
ABK52211  
ID ABK52211 standard; DNA; 33 BP.  
XX  
XX ABK52211;  
XX  
XX 13-AUG-2002 (first entry)  
XX  
XX Synthetic product 2 reverse PCR primer for construction of pASK-MBD.  
XX  
XX Mercuric ion; contaminated soil; ground water; hydroponic solution;  
KW irrigation water; waste stream; contaminated aqueous medium;  
KW biological fluid; gastrointestinal tract; chelon protein;  
KW enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;  
KW heavy metal binding protein; pASK-MBD; PCR; primer; ss.  
XX  
XX Synthetic.  
XX  
XX WO200230962-A2.  
XX  
XX 18-APR-2002.  
XX  
XX 12-OCT-2001; 2001WO-US031819.  
XX  
XX 12-OCT-2000; 2000US-0240465P.  
XX  
XX (UYGE-) UNIV GEORGIA RES FOUND INC.  
XX  
XX Summers AO, Caguiat JJ;  
XX  
XX WPI; 2002-435437/46.  
XX  
XX Novel non-naturally occurring recombinant DNA molecule encoding a chelon  
PT protein useful for binding divalent cation mercury from contaminated

PT soil, water, aqueous medium including biological fluids.  
 XX  
 PS Disclosure; Page 24; 42pp; English.  
 XX  
 CC The present invention relates to a new non-naturally occurring  
 CC recombinant DNA molecule comprising a sequence encoding a chelon protein  
 CC which binds mercuric ions. The invention is useful for recombinantly  
 CC producing a protein in a host-cell, by infecting or transforming a host  
 CC cell capable of expressing a chelon coding sequence with a vector  
 CC comprising a promoter active in the host cell operably linked to a coding  
 CC region for the protein to produce a recombinant host cell and culturing  
 CC the recombinant host cell under conditions, where DNA is expressed. The  
 CC nucleic acid encoding the chelon protein is useful for binding divalent  
 CC mercuric ions, to take up, sequester and concentrate the heavy metal ions  
 CC from contaminated soil, ground water, hydroponic solutions or irrigation  
 CC water of waste streams. The DNA of the invention, when immobilised onto a  
 CC solid support, is useful for concentrating heavy metal ions from  
 CC contaminated environment waste streams or contaminated aqueous medium  
 CC including biological fluids. The nucleic acid, when recombinantly  
 CC expressed in enteric bacteria (which are nontoxicogenic and nonpathogenic),  
 CC is suitable for use in the in vivo sequestration and elimination of  
 CC mercuric ion from gastrointestinal tracts of animals or humans exposed to  
 CC toxic metal ions such as mercury and/or cadmium. The molecules of the  
 CC invention are also useful in water treatment resins. The nucleic acid of  
 CC the invention is highly specific and binds divalent cation such as  
 CC mercury or cadmium with high affinity. The present nucleic acid sequence  
 CC represents synthetic product 2 reverse PCR primer that was used in the  
 CC methods of the invention for construction of pASK-MBD vector  
 XX  
 SQ Sequence 33 BP; 6 A; 8 C; 12 G; 7 T; 0 U; 0 Other;  
 Query Match 71.0%; Score 14.2; DB 6; Length 33;  
 Best Local Similarity 84.2%; Pred. No. 5.4e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GGGACGCGCGCTCGGTCA 19  
 ||| |||||  
 Db 6 GGGTCTCGCGCTCGGGCA 24  
 RESULT 7  
 ACH58106  
 ID ACH58106 standard; DNA; 25 BP.  
 AC ACH58106;  
 XX  
 DT 16-OCT-2003 (first entry)  
 DE  
 DE DNA target sequence #7242 useful in array for genetic analyses.  
 XX  
 KW Gene expression analysis; array; hybridisation; genetic variation;  
 KW tag-labelled compound; gene family; in situ hybridisation;  
 KW library screening; Southern hybridisation; northern hybridisation;  
 KW dot-blot hybridisation; gene sequence; mutation detection;  
 KW target sequence; probe; PCR; primer; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN US2003082596-A1.  
 XX  
 PD 01-MAY-2003.  
 XX  
 PF 08-AUG-2002; 2002US-00215112.  
 XX  
 PR 08-AUG-2001; 2001US-0311040P.  
 XX  
 PA (MITT/) MITTMANN M.  
 XX  
 PI Mittmann M;  
 XX  
 DR WPI; 2003-576608/54.  
 XX  
 PT New probe array useful e.g. for monitoring gene expression levels, for

PT analyzing genetic variations, or for hybridizing tag-labeled compounds,  
 PT comprises multiple nucleic acid probes.  
 XX  
 PS Claim 1; SEQ ID NO 7242; 9pp; English.  
 XX  
 CC The present invention relates to nucleic acid sequences that are  
 CC complementary to particular genes, and can be used as probes for a  
 CC variety of analyses such as gene expression analysis. Each probe  
 CC comprises 9 or more consecutive nucleotides from at least one of 14936  
 CC nucleotide sequences defined in the patent, or their perfect sense match,  
 CC sense mismatch, antisense match or antisense mismatch oligonucleotides.  
 CC The probes may be used in an array comprising at least 10 distinct  
 CC nucleic acid probes. The array is useful in monitoring gene expression  
 CC levels by hybridisation to a DNA library, in analysing genetic  
 CC variations, and in hybridising tag-labelled compounds. The probes are  
 CC useful for identifying family members of a gene. The probes are also  
 CC useful in situ hybridisations, in screening cDNA or genomic libraries  
 CC (or derived subclones) for additional clones containing segments of DNA  
 CC that have been previously isolated and sequenced, in Southern, northern,  
 CC or dot-blot hybridisation of genomic DNA to identify or detect the  
 CC sequence of any gene or detect specific mutations in any gene, and in  
 CC mapping the 5' termini of mRNA molecules by primer extensions. The  
 CC nucleic acid sequences of the invention are also useful as PCR primers.  
 CC The invention provides a large collection of nucleic acid sequences  
 CC complementary to particular genes with a wide range of analytical uses.  
 CC ACH50865-ACH65260 represent the target sequences of the invention. Note:  
 CC The sequence data for this patent was obtained in electronic format  
 CC directly from the USPTO web site at seqdata.uspto.gov/psipdsIDentry.html  
 XX  
 SQ Sequence 25 BP; 4 A; 9 C; 9 G; 3 T; 0 U; 0 Other;  
 Query Match 70.0%; Score 14; DB 9; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 6.8e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GGACGCGCGCTCG 15  
 |||||  
 Db 2 GGACGCGCGCTCG 15  
 |||||  
 RESULT 8  
 ACI03862/c  
 ID ACI03862 standard; DNA; 25 BP.  
 XX  
 AC ACI03862;  
 XX  
 DT 13-OCT-2003 (first entry)  
 DE  
 DE Human microarray DNA oligonucleotide SEQ ID NO 3853.  
 XX  
 KW EST; ss; probe; expressed sequence tag; microarray; gene expression;  
 KW genetic variation; biallelic marker; polymorphism; human;  
 KW cross-species comparison.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003104410-A1.  
 XX  
 PD 05-JUN-2003.  
 XX  
 PF 15-MAR-2002; 2002US-00098263.  
 XX  
 PR 16-MAR-2001; 2001US-0276759P.  
 XX  
 PA (AFFY-) AFFYMETRIX INC.  
 XX  
 PI Mittmann MP;  
 XX  
 DR WPI; 2003-567953/53.  
 XX  
 PT New array of nucleic acid probes, useful for in situ hybridization, in  
 PT Southern, Northern or dot-blot hybridization to identify or detect the  
 PT sequence or specific mutations of any gene.



XX Claim 1; SEQ ID NO 3853; 9pp; English.  
 XX  
 CC The invention discloses a microarray comprising a plurality of nucleic  
 CC acid probes including one of 2,018,500 fully defined sequences, or its  
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
 CC Also disclosed is a method of gene expression analysis. The array is used  
 CC in monitoring gene expression levels by hybridisation to a DNA library,  
 CC in analysis of genetic variation or in hybridisation of tag-labelled  
 CC compounds. The nucleic acid probes are specifically designed for analysis  
 CC of at least one target sequence. The method of analysis comprises  
 CC hybridising at least one or more nucleic acids to at least two or more  
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
 CC probes are attached to a solid support. The analysis comprises monitoring  
 CC gene expression levels, identifying allelic markers or polymorphisms,  
 CC or family members of a gene and a cross-species comparison. Each of the  
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-  
 CC blot hybridisation to identify or detect the sequence or specific  
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
 CC primer extensions or in screening cDNA or genomic libraries or subclones  
 CC for additional subclones containing segments of DNA that have been  
 CC isolated and previously sequenced. The sequence presented is one of the  
 CC nucleic acid probes incorporated in the microarray. Note: The sequence  
 CC data for this patent can also be obtained in electronic format directly  
 CC from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)  
 XX  
 SQ Sequence 25 BP; 6 A; 8 C; 8 G; 3 T; 0 U; 0 Other;  
 Query Match 66.0%; Score 13.2; DB 9; Length 25;  
 Best Local Similarity 83.3%; Pred. No. 1.6e+04;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 GGACGGCGGCTCGGTCA 19  
 Db 24 GGACTCGTGGTGGTCA 7  
 RESULT 9  
 ACI65798  
 ID ACI65798 standard; DNA; 25 BP.  
 XX  
 AC ACI65798;  
 XX  
 DT 14-OCT-2003 (first entry)  
 XX  
 DE Human microarray DNA oligonucleotide SEQ ID NO 65789.  
 XX  
 KW EST; ss; probe; expressed sequence tag; microarray; gene expression;  
 KW genetic variation; allelic marker; polymorphism; human;  
 KW cross-species comparison.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003104410-A1.  
 XX  
 PD 05-JUN-2003.  
 XX  
 PF 15-MAR-2002; 2002US-00098263.  
 XX  
 PR 16-MAR-2001; 2001US-0276759P.  
 XX  
 PA (AFFY-) AFFYMETRIX INC.  
 XX  
 PI Mitmann MP;  
 XX  
 DR WPI; 2003-567953/53.  
 XX  
 PT New array of nucleic acid probes, useful for in situ hybridization, in  
 PT Southern, Northern or dot-blot hybridization to identify or detect the  
 PT sequence or specific mutations of any gene.  
 XX  
 PS Claim 1; SEQ ID NO 65789; 9pp; English.

XX  
 CC The invention discloses a microarray comprising a plurality of nucleic  
 CC acid probes including one of 2,018,500 fully defined sequences, or its  
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
 CC Also disclosed is a method of gene expression analysis. The array is used  
 CC in monitoring gene expression levels by hybridisation to a DNA library,  
 CC in analysis of genetic variation or in hybridisation of tag-labelled  
 CC compounds. The nucleic acid probes are specifically designed for analysis  
 CC of at least one target sequence. The method of analysis comprises  
 CC hybridising at least one or more nucleic acids to at least two or more  
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
 CC probes are attached to a solid support. The analysis comprises monitoring  
 CC gene expression levels, identifying allelic markers or polymorphisms,  
 CC or family members of a gene and a cross-species comparison. Each of the  
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-  
 CC blot hybridisation to identify or detect the sequence or specific  
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
 CC primer extensions or in screening cDNA or genomic libraries or subclones  
 CC for additional subclones containing segments of DNA that have been  
 CC isolated and previously sequenced. The sequence presented is one of the  
 CC nucleic acid probes incorporated in the microarray. Note: The sequence  
 CC data for this patent can also be obtained in electronic format directly  
 CC from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)  
 XX  
 SQ Sequence 25 BP; 4 A; 8 C; 9 G; 4 T; 0 U; 0 Other;  
 Query Match 66.0%; Score 13.2; DB 9; Length 25;  
 Best Local Similarity 83.3%; Pred. No. 1.6e+04;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 GACGGCGGCTCGGTCA 20  
 Db 5 GACCGGAGCTCGGTCT 22  
 RESULT 10  
 AAH21740  
 ID AAH21740 standard; DNA; 27 BP.  
 XX  
 AC AAH21740;  
 XX  
 DT 14-AUG-2001 (first entry)  
 XX  
 DE Corynebacterium glutamicum chaperone CpkB related PCR primer SEQ.13.  
 XX  
 KW Corynebacterium glutamicum; chaperone; chaperonin; CpkB; groEL;  
 KW fermentation; L-glutamic acid; thermophilic microbe; PCR primer; ss.  
 XX  
 OS Corynebacterium glutamicum.  
 XX  
 PN JP2001069979-A.  
 XX  
 PD 21-MAR-2001.  
 XX  
 PF 31-AUG-1999; 99JP-00245121.  
 XX  
 PR 31-AUG-1999; 99JP-00245121.  
 XX  
 PA (NISR) JAPAN TOBACCO INC.  
 PA (BEAB-) BE ABLE KK.  
 XX  
 DR WPI; 2001-321175/34.  
 XX  
 PT Preparation of L-glutamic acid by fermentation.  
 XX  
 PS Example 1; Page 11; 18pp; Japanese.  
 XX  
 CC The present invention describes an L-glutamic acid-producing microbe (I)  
 CC or its mutant which expresses the molecular chaperone derived from a  
 CC thermophilic microbe and produces stably L-glutamic acid at a temperature  
 CC near the upper limit of optimum growth or higher. (I) or its mutant  
 CC transformed by a recombinant DNA containing a gene encoding the molecular

CC chaperone derived from a thermophilic microbe and a promoter operably  
 CC associated with a gene (III) comprising: (a) a fully defined 1661 base  
 CC pair (bp) sequence (AAH21757); (b) a nucleic acid sequence encoding a  
 CC protein comprising: (i) a base sequence in which 1-20 bases are deleted,  
 CC replaced or added in AAH21757; or (ii) at least one base is deleted,  
 CC having molecular chaperone activity in (i). Also described is a method  
 CC for the preparation of L-glutamic acid by fermentation in which the  
 CC transformed (I) is used and cultured at a high temperature limiting the  
 CC production of L-glutamic acid with the untransformed (I). The microbe can  
 CC be used for the preparation of L-glutamic acid. The present sequence  
 CC represents a PCR primer used in the preparation of *Corynebacterium*  
 CC glutamicum chaperone CpxB, which is used in an example from the present  
 CC invention

XX SQ Sequence 27 BP; 4 A; 9 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 66.0%; Score 13.2; DB 4; Length 27;  
 Best Local Similarity 83.3%; Pred. No. 1.6e+04;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GACGGCGCGCTCGTCAT 20  
 |||||  
 Db 9 GACGGCGCGACGGCCAT 26

RESULT 11

AAV51704/c

ID AAV51704 standard; DNA; 21 BP.

AC AAV51704;

DT 02-FEB-1999 (first entry)

DE Zea mays genome forward PCR primer #304.

XX Polymorphic marker; allele-specific; probe; amplification; PCR primer;  
 KW hybridisation; plant; hybrid certification; genetic contribution;  
 KW progeny; back-cross; hybrid; ancestry; corn; ss.

OS Synthetic.

OS Zea mays.

PN WO9824796-A1.

XX 11-JUN-1998.

PF 01-DEC-1997; 97WO-US021782.

PR 02-DEC-1996; 96US-0032069P.

PR 07-MAR-1997; 97US-00813507.

PA (AFFY-) AFFYMETRIX INC.

XX Lemieux B, Landry BS, Sapolsky RJ, Murigneux A;

XX WPI; 1998-333252/29.

XX Brassica species allele-specific oligonucleotide probes and primers -  
 PT useful for plant breeding.

PS Example 1; Page 55; 65pp; English.

XX AAV51401-V51704 are forward PCR primers used to amplify fragments of the  
 CC Zea mays genome in order to detect polymorphic markers. Such markers can  
 CC be used in the construction of allele-specific primers and probes for  
 CC amplification or hybridisation, e.g. to determine common or disparate  
 CC ancestry between 2 or more plants, to monitor the genetic contribution of  
 CC an ancestral plant, to trace the progeny of proprietary plants, in  
 CC certification of a hybrid plant or to identify the progeny of a back-  
 CC crossed plant with an ancestral plant

XX SQ Sequence 21 BP; 3 A; 11 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 2; Length 21;  
 Best Local Similarity 87.5%; Pred. No. 2.4e+04;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCGG 16  
 |||||  
 Db 16 GGGACGCGCGCTCGG 1

RESULT 12

AAW5395/c

ID AAW5395 standard; DNA; 23 BP.

XX AC AAW5395;

DT 15-JAN-2001 (first entry)

DE Fragment derived from the origin of replication of pBR322.

XX pBR322 plasmid; probe; primer; origin of replication;

XX gene therapy vector; ss.

OS Synthetic.

PN WO200053803-A1.

XX 14-SEP-2000.

PF 03-MAR-2000; 2000WO-PR000543.

PR 05-MAR-1999; 99FR-00002968.

PA (TRGE ) TRANSGENE.

XX Lamy D;

XX WPI; 2000-587445/55.

XX Nucleic acid sequences that hybridize to the pBR322 origin of  
 PT replication, useful for monitoring gene therapy vectors, and as probes or  
 PT primers.

XX Claim 3; Page 26; 36pp; French.

XX AAW5311-41 and AAW5393-A75402 are derived from the origin of  
 CC replication of the pBR322 plasmid. The nucleic acid fragments are useful  
 CC as probes and primers for detecting sequences derived from the origin of  
 CC replication of pBR322 or vectors (or their fragments) that contain such  
 CC sequences. They are particularly used to monitor the presence of gene  
 CC therapy vectors (used to deliver therapeutic genes or proteins, antisense  
 CC sequences or ribozymes), e.g. for determining disappearance of the  
 CC vector, for adjustment of treatment, or for timing of new treatments.  
 CC They can also be used to screen foods and cosmetics for the presence of  
 CC derived materials from genetically modified organisms

XX SQ Sequence 23 BP; 6 A; 7 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 3; Length 23;  
 Best Local Similarity 87.5%; Pred. No. 2.4e+04;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CGCGCGCGCTCGTCAT 20  
 |||||  
 Db 16 CGCTCGCTCGGTCGT 1

RESULT 13

ABZ58873

ID ABZ58873 standard; DNA; 24 BP.

XX AC ABZ58873;

DT 27-OCT-2003 (revised)  
 XX 28-APR-2003 (first entry)  
 DE Zebrafish ZERG mRNA inhibiting antisense oligonucleotide.  
 XX  
 KW Teleost; zebrafish; ZERG; cardiovascular; antiarrhythmic; cytostatic;  
 KW neuroprotective; gene therapy; potassium channel; antisense; ss.  
 XX  
 OS Danio rerio.  
 XX  
 XX WO2003006502-A2.  
 XX  
 XX 23-JAN-2003.  
 XX  
 XX 11-JUL-2002; 2002WO-IB004280.  
 XX  
 XX 13-JUL-2001; 2001US-0305396P.  
 XX  
 XX (ARTE-) ARTEMIS PHARM GMBH.  
 XX  
 XX Langheinrich U;  
 XX  
 XX WPI; 2003-210421/20.  
 XX  
 XX New teleost (specifically zebrafish) ERG genes, which encode ERG family  
 XX potassium channels, useful for studying e.g. cardiac or brain function,  
 XX or for developing treatments for e.g. cardiac diseases, cancer or  
 XX neurological diseases.  
 XX  
 XX Claim 7; Page 28; 55pp; English.  
 XX  
 XX The invention relates to a teleost (zebrafish) ERG (ZERG) polypeptide.  
 XX The ZERG nucleic acid molecule is useful for studying cardiac function,  
 XX abnormal heart beat phenotype, or long QT syndrome (an abnormality of  
 XX cardiac muscle repolarization that predisposes affected individuals to  
 XX lethal arrhythmias). The zebrafish comprising ZERG gene is useful as  
 XX models for cardiac function or disease. The ZERG genes are particularly  
 XX useful for in (non-)cardiac researches, or for developing treatments for  
 XX cardiac diseases, tumours or cancers, brain and nervous system disorders  
 XX or neurological diseases, or insulin-related diseases. The present  
 XX sequence represents the zebrafish ZERG mRNA inhibiting antisense  
 XX oligonucleotide. (Updated on 27-OCT-2003 to standardise OS field)  
 XX  
 SQ Sequence 24 BP; 4 A; 8 C; 9 G; 3 T; 0 U; 0 Other;  
 Query Match 64.0%; Score 12.8; DB 8; Length 24;  
 Best Local Similarity 87.5%; Pred. No. 2.4e+04;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 5 CGCGGCGCTCGGTTCAT 20  
 |||||  
 DB 9 CGCGGCGCAGGGGCAT 24  
 |||||  
 RESULT 14  
 ACI84537/c  
 ID ACI84537 standard; DNA; 25 BP.  
 XX  
 AC ACI84537;  
 XX  
 XX 14-OCT-2003 (first entry)  
 XX  
 XX Human microarray DNA oligonucleotide SEQ ID NO 84528.  
 XX  
 XX EST; ss; probe; expressed sequence tag; microarray; gene expression;  
 KW genetic variation; biallelic marker; polymorphism; human;  
 KW cross-species comparison.  
 XX  
 XX Homo sapiens.  
 OS  
 XX US2003104410-A1.  
 PN  
 XX 05-JUN-2003.  
 PD

XX 15-MAR-2002; 2002US-00098263.  
 XX  
 XX 16-MAR-2001; 2001US-0276759P.  
 PR  
 XX (AFFY-) AFFYMETRIX INC.  
 PA  
 XX Mittmann MP;  
 PI  
 XX WPI; 2003-567953/53.  
 DR  
 XX  
 XX New array of nucleic acid probes, useful for in situ hybridization, in  
 PT Southern, Northern or dot-blot hybridization to identify or detect the  
 PT sequence or specific mutations of any gene.  
 PT  
 XX Claim 1; SEQ ID NO 84528; 9pp; English.  
 PS  
 XX The invention discloses a microarray comprising a plurality of nucleic  
 CC acid probes including one of 2,018,500 fully defined sequences, or its  
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
 CC Also disclosed is a method of gene expression analysis. The array is used  
 CC in monitoring gene expression levels by hybridisation to a DNA library,  
 CC in analysis of genetic variation or in hybridisation of tag-labelled  
 CC compounds. The nucleic acid probes are specifically designed for analysis  
 CC of at least one target sequence. The method of analysis comprises  
 CC hybridising at least one or more nucleic acids to at least two or more  
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
 CC probes are attached to a solid support. The analysis comprises monitoring  
 CC gene expression levels, identifying biallelic markers or polymorphisms,  
 CC or family members of a gene and a cross-species comparison. Each of the  
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
 CC probes is useful in in situ hybridisation, in Southern, Northern or dot-  
 CC blot hybridisation to identify or detect the sequence or specific  
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
 CC primer extensions or in screening cDNA or genomic libraries or subclones  
 CC for additional subclones containing segments of DNA that have been  
 CC isolated and previously sequenced. The sequence presented is one of the  
 CC nucleic acid probes incorporated in the microarray. Note: The sequence  
 CC data for this patent can also be obtained in electronic format directly  
 CC from USPTO at seqdata.uspto.gov/sequence.html  
 XX  
 SQ Sequence 25 BP; 4 A; 9 C; 7 G; 5 T; 0 U; 0 Other;  
 Query Match 64.0%; Score 12.8; DB 9; Length 25;  
 Best Local Similarity 87.5%; Pred. No. 2.4e+04;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GGGACGCGCGCTCGG 16  
 |||||  
 DB 16 GGGACACGGCACTCGG 1  
 |||||  
 RESULT 15  
 ADO31537  
 ID ADO31537 standard; DNA; 29 BP.  
 XX  
 AC ADO31537;  
 XX  
 XX 26-AUG-2004 (first entry)  
 DT  
 XX Human CFTR gene wild-type probe for variant S549N.  
 DE  
 XX Human; CFTR gene; ss; probe; cystic fibrosis;  
 KW Cystic Fibrosis Transmembrane Conductance Regulator;  
 KW invasive cleavage structure assay; INVADER; FRET;  
 KW fluorescent resonance energy transfer; multiplexed amplification.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO2004046688-A2.  
 PN  
 XX 03-JUN-2004.  
 PD

PF 14-NOV-2003; 2003WO-US036611.  
XX  
PR 14-NOV-2002; 2002US-0426144P.  
PR 21-FEB-2003; 2003US-00371913.  
PR 26-JUN-2003; 2003US-00606577.  
PR 21-JUL-2003; 2003US-0489095P.  
PR 25-AUG-2003; 2003US-0497644P.  
PR 28-OCT-2003; 2003US-0515175P.  
PR 14-NOV-2003; 2003US-00713653.  
XX  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
XX  
XX Accola M, Wigdal SS, Mast AL, Bartholomay CT, Kwiatkowski RW;  
PI Tevere V, Ip HS, Carroll K, Peterson P, Agarwal P, Jarvis N;  
PI Hall JG, Heisler L;  
XX  
XX WPI; 2004-420702/39.  
XX  
XX  
PT Detecting Cystic Fibrosis Transmembrane Conductance Regulator (CFTR)  
PT alleles, useful for screening mutations associated with cystic fibrosis,  
PT comprises exposing amplified CFTR target nucleic acid to detection  
PT assays.  
XX  
XX Example 7; SEQ ID NO 169; 147bp; English.  
XX  
XX The invention relates to detecting Cystic Fibrosis Transmembrane  
CC Conductance Regulator (CFTR) alleles comprising providing a sample  
CC comprising a CFTR target nucleic acid, amplifying the CFTR target nucleic  
CC acid with 25 cycles or fewer of a PCR to generate amplified target  
CC nucleic acid, and exposing the amplified target nucleic acid to detection  
CC assays configured to detect CFTR alleles under conditions such that the  
CC presence or absence of the CFTR alleles is detected, using an invasive  
CC cleavage structure assay (designated INVADER), employing FRIT probes  
CC (fluorescent resonance energy transfer). Also included is a kit  
CC comprising a non-amplified oligonucleotide detection assay configured for  
CC detecting at least one CFTR allele or oligonucleotide where the set is a first  
CC configured for detecting a set of CFTR alleles where the set is a first  
CC set comprising 2789+5G to A, R1162X, R560T, 1898+1 G to A, del1507,  
CC 1148T, and A455E, a second set comprising 3120+1G to A, 3659delC, G551D,  
CC N1303K, 1078delT, R334W, 711+1G to T, and 3849+10kb, a third set  
CC comprising 621+1G to T, W1282X, 1717-1G to A, and R117H, or a fourth set  
CC comprising R347P, G85E, G542X and R553X, or a fifth set comprising  
CC 2184delA. The non-amplified oligonucleotide detection assay or the  
CC oligonucleotide detection assays comprises first and second  
CC oligonucleotides configured to form an invasive cleavage structure in  
CC combination with a target sequence comprising the CFTR allele. The first  
CC oligonucleotide comprises a 5' portion and a 3' portion, where the 3'  
CC portion is configured to hybridize to the target sequence and the 5'  
CC portion is configured to not hybridize to the target sequence. The second  
CC oligonucleotide comprises a 5' portion and a 3' portion, where the 5'  
CC portion is configured to hybridize to the target sequence and the 3'  
CC portion is configured to not hybridize to the target sequence. The method  
CC and kit are useful for detecting CFTR alleles, more particularly for  
CC screening nucleic acid samples e.g. from patients, for the presence of  
CC any one of a collection of mutations in the CFTR gene associated with  
CC cystic fibrosis. The method and compositions are useful for generating  
CC and analysing limited cycle, multiplexed amplification of a large  
CC collection of CFTR loci. The present sequence comprises a probe for the  
CC method of the invention detecting the wild-type CFTR allele.  
XX  
SQ Sequence 29 BP; 6 A; 9 C; 9 G; 5 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 12; Length 29;  
Best Local Similarity 87.5%; Pred. No. 2.4e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGACGCGGCTCGGT 17  
Db 3 GGACGCGGAGCTCAGT 18  
|||||

Search completed: May 8, 2006, 09:17:44  
Job time : 281 secs

GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2006, 10:10:02 ; Search time 357 Seconds  
(without alignments)  
228.153 Million cell updates/sec

Title: US-10-605-498-82

Perfect score: 20

Sequence: 1 gggacgcgcgcgtcggtcat 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9306428 seqs, 2036268586 residues

Total number of hits satisfying chosen parameters: 13137730

Minimum DB seq length: 0

Maximum DB seq length: 35

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_NA\_New.\*  
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2: /SIDSS/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
3: /SIDSS/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
4: /SIDSS/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*  
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13: /SIDSS/ptodata/2/pubpna/US10\_NEW\_PUB.seq4.\*  
14: /SIDSS/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
15: /SIDSS/ptodata/2/pubpna/US11\_NEW\_PUB.seq2.\*  
16: /SIDSS/ptodata/2/pubpna/US11\_NEW\_PUB.seq3.\*  
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18: /SIDSS/ptodata/2/pubpna/US11\_NEW\_PUB.seq5.\*  
19: /SIDSS/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	18	US-11-262-388-82
2	20	100.0	21	18	US-11-262-388-81
3	19	95.0	19	18	US-11-262-388-90
4	16	80.0	21	18	US-11-262-388-3
5	15.2	76.0	22	10	US-10-310-914A-649206
6	15.2	76.0	25	17	US-11-121-849-405955
7	15	75.0	21	18	US-11-262-388-4
8	14.8	74.0	23	10	US-10-310-914A-1230089
9	14.4	72.0	18	10	US-10-310-914A-940948
10	14.4	72.0	21	10	US-10-310-914A-1294776
11	14.4	72.0	22	10	US-10-310-914A-597930
12	14.4	72.0	24	10	US-10-310-914A-940913
13	14	70.0	22	10	US-10-310-914A-185611
14	13.8	69.0	24	10	US-10-310-914A-279177

15	13.8	69.0	24	10	US-10-310-914A-279178	Sequence 279178,
16	13.8	69.0	24	10	US-10-310-914A-279179	Sequence 279179,
17	13.8	69.0	24	10	US-10-310-914A-279180	Sequence 279180,
18	13.8	69.0	25	11	US-10-932-182A-16224	Sequence 16224, A
19	13.8	69.0	25	11	US-10-932-182A-16224	Sequence 16224, A
20	13.8	69.0	25	17	US-11-121-849-405692	Sequence 405692,
21	13.6	68.0	21	10	US-10-310-914A-371039	Sequence 371039,
22	13.6	68.0	21	10	US-10-310-914A-1263762	Sequence 1263762,
23	13.4	67.0	19	10	US-10-310-914A-625756	Sequence 625756,
24	13.4	67.0	20	10	US-10-310-914A-968771	Sequence 968771,
25	13.4	67.0	22	18	US-11-148-423-82	Sequence 82, Appl
26	13.4	67.0	26	10	US-10-310-914A-1239636	Sequence 1239636,
27	13.4	67.0	30	14	US-11-226-605-70	Sequence 70, Appl
28	13.2	66.0	18	10	US-10-310-914A-1303083	Sequence 1303083,
29	13.2	66.0	19	10	US-10-310-914A-41833	Sequence 41833, A
30	13.2	66.0	21	10	US-10-310-914A-615113	Sequence 615113,
31	13.2	66.0	24	10	US-10-310-914A-62912	Sequence 62912, A
32	13.2	66.0	25	10	US-10-310-914A-839926	Sequence 839926,
33	13.2	66.0	25	17	US-11-121-849-39050	Sequence 39050, A
34	13.2	66.0	25	17	US-11-121-849-143212	Sequence 143212,
35	13.2	66.0	25	17	US-11-136-527-297166	Sequence 297166,
36	13	65.0	25	11	US-10-933-982-120239	Sequence 120239,
37	13	65.0	25	11	US-10-933-982-151912	Sequence 151912,
38	13	65.0	25	11	US-10-933-982-201040	Sequence 201040,
39	13	65.0	25	11	US-10-934-048A-115670	Sequence 115670,
40	12.8	64.0	18	10	US-10-310-914A-60726	Sequence 60726, A
41	12.8	64.0	18	10	US-10-310-914A-721661	Sequence 721661,
42	12.8	64.0	19	10	US-10-310-914A-60727	Sequence 60727, A
43	12.8	64.0	19	10	US-10-310-914A-60744	Sequence 60744, A
44	12.8	64.0	19	10	US-10-310-914A-261943	Sequence 261943,
45	12.8	64.0	19	10	US-10-310-914A-984231	Sequence 984231,

ALIGNMENTS

RESULT 1

US-11-262-388-82  
; Sequence 82, Application US/11262388  
; Publication No. US2006004086A1  
; GENERAL INFORMATION:  
; APPLICANT: Gleave, Martin  
; APPLICANT: Rocchi, Palma  
; APPLICANT: Signaevsky, Maxim  
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other  
; TITLE OF INVENTION: Cancers  
; FILE REFERENCE: UBC.P-031  
; CURRENT APPLICATION NUMBER: US/11/262,388  
; CURRENT FILING DATE: 2005-10-28  
; PRIOR APPLICATION NUMBER: US/10/605,498  
; PRIOR FILING DATE: 2003-10-02  
; PRIOR APPLICATION NUMBER: US 60/415,859  
; PRIOR FILING DATE: 2002-10-02  
; PRIOR APPLICATION NUMBER: US 60/463,952  
; PRIOR FILING DATE: 2003-04-18  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 82  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-262-388-82

Query Match 100.0%; Score 20; DB 18; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCGGTCA 20

Db 1 GGGACGCGCGCTCGGTCA 20

RESULT 2

```
US-11-262-388-81
; Sequence 81, Application US/11262388
; Publication No. US20060040886A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Signaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; TITLE OF INVENTION: Cancers
; FILE REFERENCE: UBC.P-031
; CURRENT APPLICATION NUMBER: US/11/262,388
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: US/10/605,498
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-262-388-81

Query Match      100.0%; Score 20; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCGGTCAAT 20
Db 2 GGGACGCGCGCTCGGTCAAT 21

RESULT 3
US-11-262-388-90/c
; Sequence 90, Application US/11262388
; Publication No. US20060040886A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Signaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; TITLE OF INVENTION: Cancers
; FILE REFERENCE: UBC.P-031
; CURRENT APPLICATION NUMBER: US/11/262,388
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: US/10/605,498
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-262-388-90

Query Match      95.0%; Score 19; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGACGCGCGCTCGGTCAAT 20
Db 19 GGACGCGCGCTCGGTCAAT 1

RESULT 4
US-11-262-388-93
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; Sequence 3, Application US/11262388
; Publication No. US20060040886A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Signaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; TITLE OF INVENTION: Cancers
; FILE REFERENCE: UBC.P-031
; CURRENT APPLICATION NUMBER: US/11/262,388
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: US/10/605,498
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-262-388-3

Query Match      80.0%; Score 16; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGCGCGCGCTCGGTCAAT 20
Db 1 CGCGCGCGCTCGGTCAAT 16

RESULT 5
US-10-310-914A-649206/c
; Sequence 649206, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 649206
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-649206

Query Match      76.0%; Score 15.2; DB 10; Length 22;
Best Local Similarity 85.0%; Pred. No. 4.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCGGTCAAT 20
Db 21 GGGACGCGCGCTCGGTCAAT 2

RESULT 6
US-11-121-849-405955/c
; Sequence 405955, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
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TYPE: RNA

TYPE: RNA

US-10-310-914A-597930/c  
; Sequence 597930, Application US/10310914A

```
;; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 597930
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-597930

Query Match          72.0%; Score 14.4; DB 10; Length 22;
Best Local Similarity 93.8%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGACGCGGCTCGG 16
   |||||
Db 22 GGGACGCGGCTCGG 7

RESULT 12
US-10-310-914A-940913/c
; Sequence 940913, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 940913
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-940913

Query Match          72.0%; Score 14.4; DB 10; Length 24;
Best Local Similarity 93.8%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGACGCGGCTCGG 16
   |||||
Db 19 GGGACGCGGCTCGG 4

RESULT 13
US-10-310-914A-185611
; Sequence 185611, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 185611
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
```

```
US-10-310-914A-185611

Query Match          70.0%; Score 14; DB 10; Length 22;
Best Local Similarity 92.9%; Pred. No. 2e+03;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGCGGCTCGTC 14
   |||||
Db 8 GGGACGCGGCGCUC 21

RESULT 14
US-10-310-914A-279177
; Sequence 279177, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 279177
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-279177

Query Match          69.0%; Score 13.8; DB 10; Length 24;
Best Local Similarity 82.4%; Pred. No. 2.5e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGCACGCGGCTCGGTC 18
   |||||
Db 6 GGCACGCGGCGCGGUC 22

RESULT 15
US-10-310-914A-279178
; Sequence 279178, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 279178
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-279178

Query Match          69.0%; Score 13.8; DB 10; Length 24;
Best Local Similarity 82.4%; Pred. No. 2.5e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGCACGCGGCTCGGTC 18
   |||||
Db 6 GGCACGCGGCGCGGUC 22

Search completed: May 8, 2006, 10:20:49
Job time : 357 secs
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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2006, 09:37:03 ; Search time 1958 Seconds  
(without alignments)  
477.907 Million cell updates/sec

Title: US-10-605-498-82

Perfect score: 20

Sequence: 1 gggacgcggctcggtcat 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 78772

Minimum DB seq length: 0

Maximum DB seq length: 35

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST.\*

- 1: gb\_est1.\*
- 2: gb\_est2.\*
- 3: gb\_est3.\*
- 4: gb\_hc.\*
- 5: gb\_est4.\*
- 6: gb\_est5.\*
- 7: gb\_est6.\*
- 8: gb\_est7.\*
- 9: gb\_gss1.\*
- 10: gb\_gss2.\*
- 11: gb\_gss3.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	12.8	64.0	32	2	BF131807	BF131807 601820724
C 2	12.4	62.0	26	10	AG203073	AG203073 Pan trogl
C 3	12.2	61.0	28	1	AI287864	AI287864 qv07d12.x
C 4	12	60.0	31	1	AA867755	AA867755 vx16b08.r
C 5	12	60.0	31	10	C2169504	C2169504 G050C04 G
C 6	11.4	57.0	31	9	AZ826864	AZ826864 2M0102H20
C 7	11.2	56.0	23	10	AJ587908	AJ587908 Arabidops
C 8	11.2	56.0	31	6	CD028820	CD028820 mgmy006XA
C 9	11	55.0	21	9	AZ420773	AZ420773 IM0198E18
C 10	11	55.0	33	10	AJ599957	AJ599957 Arabidops
C 11	11	55.0	34	1	AA259780	AA259780 va87b10.r
C 12	10.6	53.0	25	1	AI758887	AI758887 ty94c11.x
C 13	10.6	53.0	25	6	CF643223	CF643223 D61 D08 F
C 14	10.6	53.0	29	6	CF643257	CF643257 D62 D05 F
C 15	10.6	53.0	33	10	AG216212	AG216212 Drosophil
C 16	10.6	53.0	35	6	CF298077	CF298077 7LEAF-01
C 17	10.6	53.0	35	6	CF642505	CF642505 D52 B05 F
C 18	10.6	53.0	35	3	DR108402	DR108402 JHU163B05
C 19	10.4	52.0	22	3	BM398778	BM398778 5009-0-5
C 20	10.4	52.0	26	10	CG731752	CG731752 1119143B1
C 21	10.4	52.0	27	11	TA103C01P	AL459264 T. brucei
C 22	10.4	52.0	28	1	AI256473	AI256473 ui86g06.x

23	10.4	52.0	29	9	CC456807	CC456807 SALK_1007
C 24	10.4	52.0	31	10	CG724391	CG724391 1119081A0
C 25	10.4	52.0	34	8	N55046	N55046 yz20g11.r1
C 26	10.4	52.0	34	9	AZ346691	AZ346691 IM0082103
C 27	10.2	51.0	25	1	AI002379	AI002379 qv87f02.s
C 28	10.2	51.0	27	6	CF277108	CF277108 14ETL--02
C 29	10.2	51.0	28	1	AB080287	AB080287 AB080287
C 30	10.2	51.0	28	1	AI358659	AI358659 qx60e07.x
C 31	10.2	51.0	29	1	AW246529	AW246529 2821891.3
C 32	10.2	51.0	30	1	AJ746806	AJ746806 AJ746806
C 33	10.2	51.0	30	10	CZ472135	CZ472135 d01278-5p
C 34	10.2	51.0	31	1	AA912813	AA912813 o143502.s
C 35	10.2	51.0	31	3	BI915569	BI915569 603176924
C 36	10.2	51.0	33	10	AJ600534	AJ600534 Arabidops
C 37	10.2	51.0	33	11	DME545177	DME545177 Drosophil
C 38	10.2	51.0	34	1	AA737625	AA737625 o85201.8
C 39	10.2	51.0	34	10	CG712020	CG712020 111902360
C 40	10	50.0	21	9	AZ513847	AZ513847 IM0360D08
C 41	10	50.0	22	8	DR103042	DR103042 JHU009E01
C 42	10	50.0	27	9	AZ769255	AZ769255 IM0569B17
C 43	10	50.0	30	1	AJ746842	AJ746842 AJ746842
C 44	10	50.0	30	10	CZ472687	CZ472687 d02227-3p
C 45	10	50.0	30	10	CZ488898	CZ488898 f06234-5p

ALIGNMENTS

RESULT 1  
BF131807/c

LOCUS

DEFINITION

601820724F1 NIH\_MGC\_58 Homo sapiens

CDNA sequence.

ACCESSION

BF131807

VERSION

BF131807.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Homo.

1 (bases 1 to 32)

REFERENCE

NIH-MGC http://mgc.mci.nih.gov/.

AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE

Unpublished (1999)

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov

Plate: LLCW889 row: p column: 05

High quality sequence start: 8

High quality sequence stop: 30.

FEATURES

Location/Qualifiers

1..32

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4052596"

/tissue\_type="hypertrophied"

/lab\_host="DH10B (T1 phage-resistant)"

/clone\_lib="NIH\_MGC\_58"

BF131807 32 bp mRNA linear EST 24-OCT-2000  
601820724F1 NIH\_MGC\_58 Homo sapiens CDNA clone IMAGE:4052596 5',  
mRNA sequence.

BF131807  
BF131807.1 GI:10970847  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.

1 (bases 1 to 32)  
NIH-MGC http://mgc.mci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: CLONETECH Laboratories, Inc.  
CDNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LLCW889 row: p column: 05  
High quality sequence start: 8  
High quality sequence stop: 30.

FEATURES  
Location/Qualifiers  
1..32  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4052596"  
/tissue\_type="hypertrophied"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH\_MGC\_58"

/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site\_1:  
SfiI (ggccgctggcc); Site\_2: SfiI (ggccattggcc);  
Double-stranded cDNA was prepared from cell line RNA. 5'  
and 3' adaptors were used in cloning as follows: 5'  
adaptor sequence: 5'-CACGGCATTATGGCC-3' and 3' adaptor  
sequence: 5'-ATTGAGCGCGCGGCATG-DT(30)BN-3'.  
(where B = A, C, G and N = A, C, G, or T). Average

insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN  
Query Match 64.0%; Score 12.8; DB 2; Length 32;  
Best Local Similarity 87.5%; Pred. No. 2.5e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 5 CGCGCGCTCGGTTCAT 20  
||| ||||| ||||| |||||  
Db 27 CGCTGGCTCGGTCT 12

RESULT 2  
AG203073  
LOCUS  
DEFINITION  
26 bp DNA linear GSS 06-MAR-2004  
Pan troglodytes DNA, clone: RP43-087B01.T7, genomic survey  
sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Pan troglodytes (chimpanzee)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Pan.

REFERENCE  
1  
AUTHORS  
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,  
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.  
BAC end sequences of Library RP-43  
Unpublished  
2 (bases 1 to 26)  
AUTHORS  
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,  
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.  
Direct Submission  
TITLE  
JOURNAL  
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of  
Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);  
52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea  
(E-mail: redstone@mail.krribb.re.kr, URL: http://phs.grc.krribb.re.kr/,  
Tel: 82-42-866-7181, Fax: 82-42-860-4409)  
Clones are derived from the chimpanzee BAC library RP-43. This BAC  
end was generated during the R&D process and may have higher chance  
of clone tracking errors.  
PRIMERS

Sequencing: T7  
LIBRARY  
Vector : DBACE3.6  
R.Site 1 : EcoRI  
R.Site 2 : EcoRI  
Location/Qualifiers  
1..26  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/clone="RP43-087B01.T7"  
/sex="male"  
/cell\_type="lymphocytes"  
/clone\_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN  
Query Match 62.0%; Score 12.4; DB 10; Length 26;  
Best Local Similarity 92.9%; Pred. No. 3.9e+05;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GCGACGCGCGCTC 14  
||| ||||| ||||| |||||  
Db 1 GCGACTCGCGCTC 14

RESULT 3  
AI287864/c

LOCUS  
DEFINITION

AI287864 28 bp mRNA linear EST 24-NOV-1998  
qv07dl2.xl NCI CGAP Kid8 Homo sapiens cDNA clone IMAGE:1980887 3'  
similar to SW:CA44 HUMAN P53420 COLLAGEN ALPHA 4(IV) CHAIN  
PRECURSOR. ; contains MER22.b3 TARI repetitive element ;, mRNA  
sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AI287864  
AI287864.1 GI:3927617  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 28)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers  
1..28

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1980887"  
/tissue\_type="renal cell tumor"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Kid8"  
/note="Organ: Kidney; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.2 kb. Life technologies catalog #: 11524-014"

ORIGIN

Query Match 61.0%; Score 12.2; DB 1; Length 28;  
Best Local Similarity 82.4%; Pred. No. 4.7e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGACGCGCGCTCGGT 17  
||| ||||| ||||| |||||  
Db 21 GGGCCGGGGCGCGCGT 5

RESULT 4  
AA867755/c  
LOCUS

AI287864 31 bp mRNA linear EST 16-MAR-1998  
vx16b08.r1 Soares thymus 2NbMT Mus musculus cDNA clone  
IMAGE:1264599 5' similar to TR:O35394 O35394 PRENYLATED RAB  
ACCEPTOR 1. ;, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AA867755  
AA867755.1 GI:2963200  
EST.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
1 (bases 1 to 31)  
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,



```

/db_xref="taxon:10090"
/clone="UUGC2M0102H20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 57.0%; Score 11.4; DB 9; Length 31;
Best Local Similarity 92.3%; Pred. No. 1.1e+06;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGACCGCGCGCT 13
Db 19 GGGACCGGTGCT 31

RESULT 7
AJ587908/c
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence, left border, clone 339B10, genomic survey sequence.
ACCESSION
AJ587908
VERSION
AJ587908.1 GI:37937532
KEYWORDS
GSS: left border; T-DNA flanking sequence.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eutosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
1
AUTHORS
Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G., Lepiniec,L., Caboche,M. and Lecharny,A.
T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
12446565
PUBMED
2 (bases 1 to 23)
Balzerque,S.
Direct Submission
Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
source

/db_xref="taxon:10090"
/clone="UUGC2M0102H20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 56.0%; Score 11.2; DB 10; Length 23;
Best Local Similarity 81.2%; Pred. No. 1.4e+06;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGACCGCGCGCTCGG 16
Db 21 GGGACCGCGCATGG 6

RESULT 8
CD028820
LOCUS
DEFINITION
mgy006xA17f.b Magnaporthe grisea MY Uni-Zap XR Library Magnaporthe grisea CDNA clone mgy006xA17 5', mRNA sequence.
ACCESSION
CD028820
VERSION
CD028820.1 GI:30410276
KEYWORDS
EST.
SOURCE
Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM
Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE
1 (bases 1 to 31)
AUTHORS
Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G., Bhatterai,K. and Dean,R.A.
Expressed sequence tags from the rice blast fungus, Magnaporthe grisea
Unpublished (2002)
Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact person;
PCR Primers
FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgy006 row: A column: 17
Seq primer: T3.
Location/Qualifiers
source
1..31
/organism="Magnaporthe grisea"
/mol_type="mRNA"
/strains="70-15"
/db_xref="taxon:148305"
/clone="mgy006xA17"
/sex="Mati-2 hermaphrodite"
/cell_type="mycelium"
/clone_lib="Magnaporthe grisea MY Uni-Zap XR Library"
/notes="Vector: pBluescriptSK+; Site_1: EcoRI; Site_2: XhoI; Unidirectional cloning, EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Minimal medium mycelium library. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."

```

## ORIGIN

Query Match 56.0%; Score 11.2; DB 6; Length 31;  
 Best Local Similarity 81.2%; Pred. No. 1.3e+06;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CGCGGGCTCGGTTCAT 20  
 |||||  
 Db 6 CTCGGCGTTGGTTCAT 21

## RESULT 9

AZ420773/c  
 LOCUS  
 DEFINITION 21 bp DNA linear GSS 03-OCT-2000  
 1M0198E18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0198E18 R, genomic survey sequence.

ACCESSION AZ420773.1 GI:10544786  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 21)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.

## TITLE

Muscle whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

## JOURNAL

Unpublished (2000)

## COMMENT

Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0198 row: E column: 18

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

## FEATURES

Location/Qualifiers

1..21

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0198E18"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

## ORIGIN

Query Match 55.0%; Score 11; DB 9; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGCGCGC 11  
 |||||

Db 16 GGGACGCGCGC 6

## RESULT 10

AJ599957

LOCUS

DEFINITION

Arabidopsis thaliana T-DNA flanking sequence, left border, clone

497C08, genomic survey sequence.

ACCESSION AJ599957.1 GI:37949585

VERSION

KEYWORDS GSS; left border; T-DNA flanking sequence.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

## REFERENCE

1  
 Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F.,  
 Chauvin, S., Reichtold, N., Cruaud, C., DeRose, R., Pelletier, G.,  
 Lepiniec, L., Caboche, M. and Lecharny, A.

T-DNA integration into the Arabidopsis genome depends on sequences

of pre-insertion sites

EMBO Rep. 3 (12), 1152-1157 (2002)

12446565

2 (bases 1 to 33)

Authors

Direct Submission

Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue

Gaston Cremieux, 91057 Evry cedex, FRANCE

PCR was performed on DNA from transformants of Arabidopsis thaliana

plants from INRA (Versailles). The DNA fragment(s) resulting from

the PCR were directly sequenced from the left or the right border

to determine the genomic sequence flanking the insertion. T-DNA

derived sequences were removed. Information to order the

corresponding mutant line and a link to a database providing a

graphical display of the insertion site are available at

http://dbsgap.versailles.inra.fr/publiclines/. This sequence has

been generated in the framework of the French plant genomics

program 'Genoplante' (http://www.genoplante.com and

http://genoplante-info.infobiogen.fr).

## FEATURES

source

1..33

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/db\_xref="taxon:3702"

/clone="497C08"

/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"

/ecotype="Wassilewskija"

misc\_feature

1..33

/note="T-DNA flanking sequence

left border"

## ORIGIN

Query Match 55.0%; Score 11; DB 10; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGCGCGC 11  
 |||||

Db 23 GGGACGCGCGC 33

## RESULT 11

AA259780/c

and selected for ampicillin resistance."

```

LOCUS      AA259780                      34 bp      mRNA      linear      EST 18-MAR-1997
DEFINITION Va87b10.r1 Soares mouse 3NWE12.5 Mus musculus cDNA clone
            IMAGE:746395 5' similar to TR:G971986 G971986 NADH DEHYDROGENASE ;,
            mRNA sequence.
ACCESSION  AA259780
VERSION    AA259780.1 GI:1896266
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 34)
AUTHORS    Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
TITLE      The WashU-HMI Mouse EST Project
JOURNAL    Unpublished (1996)
COMMENT    Contact: Marra M/Mouse EST Project
            WashU-HMI Mouse EST Project
            Washington University School
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:455379
FEATURES   Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Seq primer: -28ml3 rev2 ET from Amersham
            High quality sequence stop: 1.
            Location/Qualifiers
                1..34
                /organism="Mus musculus"
                /mol_type="mRNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="IMAGE:746395"
                /sex="unknown"
                /tissue_type="fetus"
                /dev_stage="12.5dpc total fetus"
                /lab_host="DH10B"
                /clone_lib="Soares mouse 3NWE12 5"
                /note="Organ: whole fetus; Vector: pT7T3D-Pac (Pharmacia)
            with a modified polylinker; Site 1: Not I; Site 2: Eco RI;
            1st strand cDNA was primed with a Not I - oligo(dT) primer
            [5' TGTTACCAATCTGAGTGGAGCGCGCCCTATTTTCTTTTCTTTT
            3'], on total mouse RNA [provided by Minoru Ko, Wayne
            State Univ.]; double-stranded cDNA was ligated to Eco RI
            adaptors (Pharmacia), digested with Not I and cloned into
            the Not I and Eco RI sites of the modified pT7T3 vector.
            Library went through one round of normalization, and was
            constructed by Bento Soares and M. Fatima Bonaldo. "
ORIGIN
Query Match      55.0%; Score 11; DB 1; Length 34;
Best Local Similarity 73.7%; Pred. No. 1.6e+06;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  1 GGGACGGCGGCTCGTCA 19
    ||||| ||| |||||
DB   34 GGGACTCAGCTCATGCTCA 16

RESULT 12
AI758887      25 bp      mRNA      linear      EST 23-JUN-1999
LOCUS        ty94c11.x1 NCI CGAP Utl Homo sapiens cDNA clone IMAGE:2286740 3',
DEFINITION   similar to TR:Q64371 Q64371 PR-VBETAL. ;contains element TAR1
            repetitive element ;, mRNA sequence.
ACCESSION  AI758887
VERSION    AI758887.1 GI:5152612
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1 (bases 1 to 25)
AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
JOURNAL    Contact: Robert Strausberg, Ph.D.
            Email: c9pbbs-remail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            www-bio.llnl.gov/bbrp/image/image.html
            Trace considered overall poor quality
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
            Location/Qualifiers
                1..25
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:2286740"
                /tissue_type="well-differentiated endometrial
            adenocarcinoma, 7 pooled tumors"
                /lab_host="DH10B"
                /clone_lib="NCI CGAP Utl"
                /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
            Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
            Average insert size 1.75 kb. Life Technologies catalog #:
            11538-014"
ORIGIN
Query Match      53.0%; Score 10.6; DB 1; Length 25;
Best Local Similarity 76.5%; Pred. No. 2.5e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY  1 GGGACGGCGGCTCGGT 17
    ||| ||||| |||||
DB   5 GGGGGGGCGCGCGCGGT 21

RESULT 13
CF643223/c
LOCUS        CF643223 25 bp      mRNA      linear      EST 02-OCT-2003
DEFINITION   D61_D08 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA
            sequence.
ACCESSION  CF643223
VERSION    CF643223.1 GI:37411328
KEYWORDS   EST.
SOURCE     Ustilago maydis
ORGANISM   Ustilago maydis
            Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
            Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
REFERENCE  1 (bases 1 to 25)
AUTHORS    Nugent,K.G., Choffe,K. and Saville,B.J.
TITLE      Gene expression during Ustilago maydis diploid filamentous growth:
            EST library creation and analyses
JOURNAL     Fungal Genet. Biol. 41 (3), 349-360 (2004)
PUBMED      14761795
COMMENT     Contact: Barry J. Saville
            Saville Lab
            University of Toronto

```

3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada  
Tel: 905 569 4702  
Fax: 905 828 3792  
Email: bsaville@utm.utoronto.ca  
Plate: UTM-UM-D126/7-061-UTM row: 08 column: D  
Seq primer: T7 Reverse (5' GAGTAATACGACTCACTATAGG 3')  
High quality sequence stop: 25.  
Location/Qualifiers

## FEATURES

source

1. .25

/organism="Ustilago maydis"  
/mol\_type="mRNA"  
/strain="FBD12"  
/db\_xref="taxon:5270"  
/cell\_type="Mycelia"  
/dev\_stage="Filamentous diploid"  
/clone\_lib="Filamentous Forced Diploid"  
/notes="Vector: pSport; mRNA was extracted from diploid mycelia. A cDNA library was constructed and unidirectionally cloned into pSPORT plasmid, with the use of the Superscript II cDNA Library Construction Kit."

## ORIGIN

Query Match 53.0%; Score 10.6; DB 6; Length 25;  
Best Local Similarity 76.5%; Pred. No. 2.5e+06;  
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGACGGCGGCTCGGTC 18

|||||

Db 24 GGACGGCTGGTCGATC 8

## RESULT 14

CF643257/c

LOCUS

DEFINITION D62\_B05 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Ustilago maydis  
Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;  
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.  
1 (bases 1 to 29)  
Nugent, K.G., Choffe, K. and Saville, B.J.  
Gene expression during Ustilago maydis diploid filamentous growth:  
EST library creation and analyses

JOURNAL

PUBLISHED

COMMENT

14761795  
Fungal Genet. Biol. 41 (3), 349-360 (2004)  
Contact: Barry J. Saville  
Saville Lab  
University of Toronto  
3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada  
Tel: 905 569 4702  
Fax: 905 828 3792  
Email: bsaville@utm.utoronto.ca  
Plate: UTM-UM-D126/7-062-UTM row: 05 column: B  
Seq primer: T7 Reverse (5' GAGTAATACGACTCACTATAGG 3')  
High quality sequence stop: 29.  
Location/Qualifiers

## FEATURES

source

1. .29

/organism="Ustilago maydis"  
/mol\_type="mRNA"  
/strain="FBD12"  
/db\_xref="taxon:5270"  
/cell\_type="Mycelia"  
/dev\_stage="Filamentous diploid"  
/clone\_lib="Filamentous Forced Diploid"  
/notes="Vector: pSport; mRNA was extracted from diploid mycelia. A cDNA library was constructed and unidirectionally cloned into pSPORT plasmid, with the use of the Superscript II cDNA Library Construction Kit."

## ORIGIN

Query Match 53.0%; Score 10.6; DB 6; Length 29;  
Best Local Similarity 76.5%; Pred. No. 2.5e+06;  
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGACGGCGGCTCGGTC 18

|||||

Db 28 GGACGGCTGGTCGATC 12

## FEATURES

source

15

AG216212/c

LOCUS

DEFINITION Drosophila melanogaster DNA, clone:NP1197-5-1, flanking P[GawB]

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AG216212 33 bp DNA linear GSS 03-SEP-2002  
Drosophila melanogaster DNA, clone:NP1197-5-1, flanking P[GawB]  
transposon insertion, genomic survey sequence.  
AG216212  
AG216212.1 GI:22763212  
GSS.  
Drosophila melanogaster (fruit fly)  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.

## REFERENCE

AUTHORS

1  
Hayashi, S., Ito, K., Sado, Y., Taniguchi, M., Akimoto, A., Takeuchi, H.,  
Aigaki, T., Matsuzaki, F., Nakagoshi, H., Tanimura, T., Ueda, R.,  
Uemura, T., Yoshihara, M. and Goto, S.  
GETDB, a database compiling expression patterns and molecular  
locations of a collection of Gal4 enhancer traps  
Genesis (2002) In press  
2 (bases 1 to 33)  
Hayashi, S.  
Direct Submission

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .33

/organism="Drosophila melanogaster"

/mol\_type="genomic DNA"

/strain="NP1197"

/db\_xref="taxon:7227"

/chromosome="2"

/map="54C6"

/clone="NP1197-5-1"

/note="flanking P[GawB] transposon insertion"

ORIGIN

Query Match

Best Local Similarity

Matches

13; Conservative

0; Mismatches

4; Indels

0; Gaps

0;

QY 2 GGACGGCGGCTCGGTC 18

|||||

Db 22 GCATCGTCGACGGTC 6

Search completed: May 8, 2006, 10:09:50

Job time : 1959 secs

**HIS PAGE BLANK (USPTO)**



GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2006, 09:47:57 ; Search time 96 Seconds  
(without alignments)  
370.325 Million cell updates/sec

Title: US-10-605-498-82

Perfect score: 20

Sequence: 1 gggacggcgctcggtcat 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 889780828 residues

Total number of hits satisfying chosen parameters: 1097522

Minimum DB seq length: 0

Maximum DB seq length: 35

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents NA.\*

- 1: /cgn2\_6/ptodata/1/ina/1 COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/ina/5 COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/H COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/PTUS COMB.seq.\*
- 7: /cgn2\_6/ptodata/1/ina/PP COMB.seq.\*
- 8: /cgn2\_6/ptodata/1/ina/RE COMB.seq.\*
- 9: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.2	71.0	33	3	US-09-977-137A-16
C 2	14	70.0	25	3	Sequence 16, Appl
C 3	13.8	69.0	25	3	Sequence 42173, A
C 4	13.8	69.0	25	3	Sequence 46323, A
C 5	13.8	69.0	25	3	Sequence 46324, A
C 6	13.2	66.0	25	3	Sequence 46335, A
7	13	65.0	20	3	Sequence 53301, A
8	13	65.0	20	3	Sequence 19, Appl
9	13	65.0	20	3	Sequence 19, Appl
10	12.6	63.0	20	3	Sequence 8773, Ap
C 11	12.6	63.0	24	3	Sequence 35, Appl
C 12	12.6	63.0	24	3	Sequence 12, Appl
C 13	12.6	63.0	24	3	Sequence 14, Appl
C 14	12.6	63.0	24	3	Sequence 35, Appl
C 15	12.6	63.0	25	3	Sequence 40648, A
C 16	12.6	63.0	30	3	Sequence 52, Appl
17	12.6	63.0	30	9	Patent No. 5240848
18	12.4	62.0	20	2	US-08-182-175A-9
19	12.4	62.0	20	2	US-08-474-633A-16
20	12.4	62.0	20	3	US-08-823-771-16
21	12.4	62.0	20	6	PCT-US92-06412-9
C 22	12.4	62.0	25	3	US-09-396-196G-41065
C 23	12.4	62.0	25	3	US-09-396-196G-46162
C 24	12.4	62.0	25	3	US-09-396-196G-46163

25	12.2	61.0	21	3	US-09-158-863C-38	Sequence 38, Appl
C 26	12.2	61.0	22	3	US-09-589-560B-58	Sequence 58, Appl
C 27	12.2	61.0	22	3	US-09-589-560B-62	Sequence 62, Appl
C 28	12.2	61.0	25	3	US-09-396-196G-25195	Sequence 25195, A
C 29	12.2	61.0	25	3	US-09-396-196G-49392	Sequence 49392, A
C 30	12.2	61.0	34	3	US-09-487-558B-3	Sequence 3, Appli
C 31	12	60.0	23	3	US-09-462-671-1	Sequence 1, Appli
C 32	12	60.0	27	3	US-08-485-355B-4	Sequence 4, Appli
C 33	12	60.0	29	3	US-09-045-583-45	Sequence 45, Appl
C 34	12	60.0	29	3	US-09-534-185-45	Sequence 45, Appl
C 35	12	60.0	32	3	US-08-485-355B-30	Sequence 30, Appl
C 36	12	60.0	32	3	US-09-045-583-44	Sequence 44, Appl
C 37	12	60.0	32	3	US-09-534-185-44	Sequence 44, Appl
C 38	11.8	59.0	17	2	US-08-171-299B-6	Sequence 6, Appli
C 39	11.8	59.0	20	3	US-09-467-642-13	Sequence 13, Appl
C 40	11.8	59.0	23	3	US-08-930-797B-2	Sequence 2, Appli
C 41	11.8	59.0	27	2	US-08-580-401-5	Sequence 5, Appli
C 42	11.8	59.0	27	2	US-08-927-394-8	Sequence 8, Appli
C 43	11.8	59.0	31	2	US-08-927-394-7	Sequence 7, Appli
C 44	11.6	58.0	18	3	US-09-402-618B-75	Sequence 75, Appl
C 45	11.6	58.0	18	3	US-09-942-588A-31	Sequence 31, Appl

#### ALIGNMENTS

##### RESULT 1

US-09-977-137A-16  
; Sequence 16, Application US/09977137A  
; Patent No. 6750042  
; GENERAL INFORMATION:  
; APPLICANT: Summers, Anne O.  
; APPLICANT: Caquiati, Jonathan  
; TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and  
; TITLE OF INVENTION: Methods  
; FILE REFERENCE: 79-00  
; CURRENT APPLICATION NUMBER: US/09/977,137A  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 60/240,465  
; PRIOR FILING DATE: 2000-10-12  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 33  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
US-09-977-137A-16

Query Match 71.0%; Score 14.2; DB 3; Length 33;  
Best Local Similarity 84.2%; Pred. No. 3e+03; 3; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 3;

QY 1 GGGACGCGCGCTCGGTCA 19  
||| ||||| ||||| |||||  
Db 6 GGGTCTCGCGCTCGGGCA 24

##### RESULT 2

US-09-396-196G-42173/c  
; Sequence 42173, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678

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; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42173
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-42173

Query Match          70.0%; Score 14; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CGCGCGCTCGGTTCAT 20
Db 20 CGCGCGCTCGGTTCAT 7

RESULT 3
US-09-396-196G-46323/c
; Sequence 46323, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46323
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-46323

Query Match          69.0%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ACGCGCGCTCGGTTCAT 20
Db 20 ACGCTGCGCACGCTCAT 4

RESULT 4
US-09-396-196G-46324/c
; Sequence 46324, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46324
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-46324

Query Match          69.0%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ACGCGCGCTCGGTTCAT 20
Db 20 ACGCTGCGCACGCTCAT 4

RESULT 5
US-09-396-196G-46335/c
; Sequence 46335, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46335
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-46335

Query Match          69.0%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ACGCGCGCTCGGTTCAT 20
Db 19 ACGCTGCGCACGCTCAT 3

RESULT 6
US-09-396-196G-53301
; Sequence 53301, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53301
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-53301

Query Match          66.0%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 8.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GACCGCGCGCTCGGTTCAT 20
Db 2 GACCCAGCGCTCTGTTCAT 19
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```
RESULT 7
US-09-046-858A-19
; Sequence 19, Application US/09046858A
; Patent No. 6048973
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: SUGAR-REGULATORY SEQUENCES
; IN ALPHA-AMYLASE GENES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: PO Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,858A
; FILING DATE: 24-MAR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/042,376
; FILING DATE: 24-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Dehlinger, Peter J.
; REGISTRATION NUMBER: 28,006
; REFERENCE/DOCKET NUMBER: 2000-0456.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-046-858A-19
Query Match 65.0%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GACGCGGCGCTCG 15
Db 2 GACGCGGCGCTCG 14

RESULT 8
US-09-046-858A-19
; Sequence 19, Application US/09450515
; Patent No. 6680425
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: SUGAR-REGULATORY SEQUENCES
; IN ALPHA-AMYLASE GENES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: PO Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/206,654
; FILING DATE: 25-JUL-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,858A
; FILING DATE: 24-MAR-1998
; APPLICATION NUMBER: 60/042,376
; FILING DATE: 24-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Dehlinger, Peter J.
; REGISTRATION NUMBER: 28,006
; REFERENCE/DOCKET NUMBER: 2000-0456.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-046-858A-19
Query Match 65.0%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GACGCGGCGCTCG 15
Db 2 GACGCGGCGCTCG 14

RESULT 9
US-10-206-654-19
; Sequence 19, Application US/10206654
; Patent No. 6919493
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: SUGAR-REGULATORY SEQUENCES
; IN ALPHA-AMYLASE GENES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: PO Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/206,654
; FILING DATE: 25-JUL-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,858A
; FILING DATE: 24-MAR-1998
; APPLICATION NUMBER: 60/042,376
; FILING DATE: 24-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Dehlinger, Peter J.
; REGISTRATION NUMBER: 28,006
; REFERENCE/DOCKET NUMBER: 2000-0456.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-450-515-19
Query Match 65.0%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GACGCGGCGCTCG 15
Db 2 GACGCGGCGCTCG 14
```

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-206-654-19

Query Match          65.0%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GACGCGCGCTCG 15
Db 2 GACGCGCGCTCG 14

RESULT 10
US-10-131-827-8773
; Sequence 8773, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: CHRONIC INFLAMMATORY DISEASES
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8773
; TYPE: DNA
; ORGANISM: Human cytomegalovirus
US-10-131-827-8773

Query Match          63.0%; Score 12.6; DB 3; Length 20;
Best Local Similarity 78.9%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGACGGCGCGCTCGGTTCAT 20
Db 1 GTACGGCGCTCGGTTCAT 19

RESULT 11
US-09-540-014-35/c
; Sequence 35, Application US/09540014
; Patent No. 6380372
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillaud, Maxime
; APPLICANT: Lemauz, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioresdoxin and
; FILE REFERENCE: NADP-Thioresdoxin Reductase
; CURRENT APPLICATION NUMBER: US/09/540,014
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
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; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-540-014-35

Query Match          63.0%; Score 12.6; DB 3; Length 24;
Best Local Similarity 78.9%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGACGGCGCGCTCGGTTCAT 20
Db 19 GCACGAGCGCTCGGATAT 1

RESULT 12
US-09-164-210-12/c
; Sequence 12, Application US/09164210
; Patent No. 6642437
; GENERAL INFORMATION:
; APPLICANT: P. G. Lemaux et al.
; TITLE OF INVENTION: Production of proteins in plant seeds
; FILE REFERENCE: 48722
; CURRENT APPLICATION NUMBER: US/09/164,210
; CURRENT FILING DATE: 1998-09-30
; EARLIER APPLICATION NUMBER: 09/164,210
; PRIOR FILING DATE: 1998-09-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR primer
US-09-164-210-12

Query Match          63.0%; Score 12.6; DB 3; Length 24;
Best Local Similarity 78.9%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGACGGCGCGCTCGGTTCAT 20
Db 19 GCACGAGCGCTCGGATAT 1

RESULT 13
US-09-538-864-14/c
; Sequence 14, Application US/09538864
; Patent No. 6784346
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Lemaux, Peggy G.
; APPLICANT: Buchanan, Bob B.
; APPLICANT: Wong, Joshua
; APPLICANT: Marx, Corina
; TITLE OF INVENTION: Value-Added Traits in Grain and Seed
; FILE REFERENCE: 2001-0703.30
; CURRENT APPLICATION NUMBER: US/09/538,864
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/126,736
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
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; PRIOR APPLICATION NUMBER: US 60/177,740  
; PRIOR FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: US 60/177,739  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: primer  
US-09-538-864-14

Query Match 63.0%; Score 12.6; DB 3; Length 24;  
Best Local Similarity 78.9%; Pred. No. 1.5e+04;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGACGGCGCGCTCGGTCAAT 20  
| | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 19 GCACGAGCGCGCTCGGATAT 1

RESULT 14  
US-10-091-841A-35/c  
; Sequence 35, Application US/10091841A  
; Patent No. 6833493  
; GENERAL INFORMATION:  
; APPLICANT: Cho, Myeong-Je  
; APPLICANT: del Val, Gregorio  
; APPLICANT: Caillaud, Maxime  
; APPLICANT: Lemaux, Peggy G.  
; APPLICANT: Buchanan, Bob B.  
; TITLE OF INVENTION: BARLEY GENE FOR THIOREDOXIN AND  
; TITLE OF INVENTION: NADP-THIOREDOXIN REDUCTASE  
; FILE REFERENCE: 416272001410  
; CURRENT APPLICATION NUMBER: US/10/091,841A  
; CURRENT FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: US 09/540,014  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: US 60/127,198  
; PRIOR FILING DATE: 1999-03-31  
; PRIOR APPLICATION NUMBER: US 60/169,162  
; PRIOR FILING DATE: 1999-12-06  
; PRIOR APPLICATION NUMBER: US 60/177,740  
; PRIOR FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: US 60/177,739  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 35  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: primer  
US-10-091-841A-35

Query Match 63.0%; Score 12.6; DB 3; Length 24;  
Best Local Similarity 78.9%; Pred. No. 1.5e+04;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGACGGCGCGCTCGGTCAAT 20  
| | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 19 GCACGAGCGCGCTCGGATAT 1

RESULT 15  
US-09-396-196G-40648/c  
; Sequence 40648, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann

; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 40648  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-396-196G-40648

Query Match 63.0%; Score 12.6; DB 3; Length 25;  
Best Local Similarity 78.9%; Pred. No. 1.5e+04;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGACGGCGCGCTCGGTCAAT 20  
| | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 25 GCACGGCGCGCTCGATCAT 7

Search completed: May 8, 2006, 09:49:41  
Job time : 97 secs

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